CLAIMS AMENDMENT

Claims 1-17 (Canceled).

Claim 18 (Currently amended). A method for the identification of an intramer capable of binding to and modifying the function of a functional intracellular target by a mechanism different from an antisense mechanism, comprising:

a) preparing a candidate intramer mixture of nucleic acids;

b) contacting the candidate intramer mixture of nucleic acids with the intracellular target or part thereof whereby the target or the part thereof is not known to bind RNA prior to step (b);

c) selecting and isolating nucleic acids having an increased affinity to said target reactive to the candidate intramer mixture;

d) reverse transcribing, if the candidate intramer mixture comprises RNAs, and amplifying the nucleic acids obtained in step (c);

e) optionally repeating steps (b) to (d);

f) isolating and sequencing the clones (intramers) obtained in step (e); and

g) testing whether the expression product of the insert of the clone obtained in step (f) binds to and affects the function of the intracellular target *in vivo*.

Claim 19 (Canceled).

Claim 20 (Currently amended). The method of claim~~s~~ 18 ~~or 19~~ further comprising:

h) mapping of the binding site of the intramer to said target.

Claim 21 (Currently amended). A method for the identification of a functional intracellular target which is associated with a particular phenotype and the corresponding intramer capable of binding to and modifying the function of said target by a mechanism different from an antisense mechanism, comprising:

a) preparing a candidate intramer mixture of nucleic acids;

b) cloning the candidate intramer mixture of nucleic acids under the control of a suitable promoter in a vector optionally containing a selectable marker;

c) introducing the vector obtained in step (b) into a reporter cell line allowing the positive or negative phenotype selection;

d) selecting cells with an altered phenotype; and

e) determining the sequence of the nucleic acid inserted in the vector of step (b) (intramer) and the compound to which it binds.

Claim 22 (Currently amended). The method of claim~~s 18, 19, 20 or~~ 21, wherein said candidate intramer mixture of nucleic acids comprises single stranded nucleic acids.

Claim 23 (Currently amended). The method of claim 22, wherein the single stranded nucleic acid is an RNA.

Claim 24 (Currently amended). The method of claim~~s 18, 19, 20, 21, 22 or 23,~~ 21, wherein the functional intracellular target is an integrin.

Claim 25 (Currently amended). The method of claim~~s~~ 21~~, 22, 23 or 24~~, wherein the reporter cell line of step (c) allows negative selection.

Claim 26 (Currently amended). The method of claim 25, wherein the reporter cell line contains a vector comprising a selectable marker and a reporter gene encoding a toxin under the control of an inducible ~~promotor~~ promoter and wherein the only cells that ~~will~~ survive are those that expressing the vector of step (b) which expresses a nucleic acid (intramer) inhibiting a compound which is required for the activation of the ~~promotor~~ promoter controlling the toxin gene, and wherein in step (d) the surviving cells are selected.

Claim 27 (Currently amended). The method of claim~~s~~ 21~~, 22, 23, 24, 25 or 26~~, wherein the candidate intramer mixture of nucleic acids of the vector of step (b) is under control of a Pol III promoter.

Claim 28 (Currently amended). The method of claim~~s~~ 26 ~~or 27~~, wherein the toxin gene is HSV-thymidinekinase.

Claim 29 (Currently amended). The method of claim~~s~~ ~~18, 19, 20, 21, 22, 23, 24, 25 or~~ 26, wherein the ~~promotor~~ promoter controlling the toxin gene is an IL-2 promoter.

Claim 30-35 (Canceled).

Claim 36 (New). The method of claim 18, wherein said candidate intramer mixture of nucleic acids comprises single-stranded nucleic acids.

Claim 37 (New). The method of claim 36, wherein the single-stranded nucleic acid is an RNA.

Claim 38 (New). The method of claim 18, wherein the functional intracellular target is an integrin.